

16
Rec'd PCT/PTO 06 FEB 2008
10/528631

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.

Application Serial Number: 10/528,631
Source: PG
Date Processed by STIC: 2/16/06

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PCT

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DATE: 02/16/2006

PATENT APPLICATION: US/10/528,631

TIME: 12:47:55

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Output Set: N:\CRF4\02162006\J528631.raw

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3 <110> APPLICANT: FMC Corporation
4     CHEN, Ruihua
5     HALLING, Blaik P.
6     CHAGUTURU, Munirathan K.
7     ALLENZA, Paul
8     YUHAS, Debra A.
10 <120> TITLE OF INVENTION: Hemipteran Myosin Light Chain Kinase
12 <130> FILE REFERENCE: 60289-USA
14 <140> CURRENT APPLICATION NUMBER: 10/528,631
C--> 15 <141> CURRENT FILING DATE: 2005-03-22
17 <150> PRIOR APPLICATION NUMBER: 60/413,720
18 <151> PRIOR FILING DATE: 2002-09-26
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2517
26 <212> TYPE: DNA
27 <213> ORGANISM: Aphis gossypii
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34 gaaactggca aaaaaattag aggaaaagca gatggcaata ttaaagatta cgaccaatat    180
36 gtttttgaca tttattcaaa atacatacca caaccagtgg atattaaaac acaatccgta    240
38 tatgattatt atgacatatt agaagaaatc ggaactgggt catttgaggt agtacaccgt    300
40 tgtagggaac gtaaaactgg aaatatTTTT gctgccaaat ttataccagt agcacataat    360
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78 gctgaaaata cctatggcta tagggaagaa gtcgtattcc tcaacgtaca acctttgcca 1500
80 aaagcagcac cggatatacag acatgaagtc caacaagtca gaagacgaga accactcgct 1560
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115 <210> SEQ ID NO: 2

116 <211> LENGTH: 839

117 <212> TYPE: PRT

118 <213> ORGANISM: Aphis gossypii

120 <400> SEQUENCE: 2

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123 1 5 10 15
126 Glu Val Ser Pro Ile Val Lys Thr Lys Glu Leu Leu Lys Lys Pro Pro
127 20 25 30
130 Lys Thr Lys Arg Tyr Glu Val Asp Glu Thr Gly Lys Lys Ile Arg Gly
131 35 40 45
134 Lys Ala Asp Gly Asn Ile Lys Asp Tyr Asp Gln Tyr Val Phe Asp Ile
135 50 55 60
138 Tyr Ser Lys Tyr Ile Pro Gln Pro Val Asp Ile Lys Thr Gln Ser Val
139 65 70 75 80
142 Tyr Asp Tyr Tyr Asp Ile Leu Glu Glu Ile Gly Thr Gly Ala Phe Gly
143 85 90 95
146 Val Val His Arg Cys Arg Glu Arg Lys Thr Gly Asn Ile Phe Ala Ala
147 100 105 110
150 Lys Phe Ile Pro Val Ala His Asn Val Glu Lys Glu Leu Ile Lys Lys
151 115 120 125
154 Glu Ile Asp Ile Met Asn Gln Leu His His Pro Lys Leu Ile Asn Leu
155 130 135 140
158 His Asp Ala Phe Glu Asp Glu Asp Glu Met Val Leu Ile Phe Glu Phe
159 145 150 155 160
162 Leu Ser Gly Gly Glu Leu Phe Glu Arg Ile Thr Ser Glu Gly Tyr Ser
163 165 170 175
166 Met Ser Glu Ala Glu Val Ile Asn Tyr Met Arg Gln Ile Cys Glu Ala
167 180 185 190
170 Ile Lys His Met His Glu Arg Asn Ile Ile His Leu Asp Ile Lys Pro
171 195 200 205

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174 Glu Asn Ile Met Cys Gln Thr Lys Lys Ser Ser Asn Val Lys Leu Ile
175      210                      215                      220
178 Asp Phe Gly Leu Ala Thr Lys Leu Asp Pro Asn Glu Ile Val Lys Ile
179 225                      230                      235                      240
182 Ser Thr Gly Thr Ala Glu Phe Ala Ala Pro Glu Ile Val Glu Arg Glu
183                      245                      250                      255
186 Pro Val Gly Phe Tyr Thr Asp Met Trp Ala Val Gly Val Leu Ala Tyr
187                      260                      265                      270
190 Val Leu Leu Ser Gly Leu Ser Pro Phe Ala Gly Glu Asn Asp Val Glu
191                      275                      280                      285
194 Thr Leu Lys Asn Val Lys Ala Cys Asp Trp Asp Phe Asp Glu Asp Thr
195      290                      295                      300
198 Phe Asn Ile Val Ser Asp Glu Gly Lys Asp Phe Ile Arg Arg Leu Leu
199 305                      310                      315                      320
202 Ile Lys Asn Lys Glu Lys Arg Met Thr Ala His Glu Cys Leu Ile His
203                      325                      330                      335
206 Pro Trp Leu Met Gly Asp His Ser Asp Arg Thr Ala Ala Leu Asn Ser
207                      340                      345                      350
210 Ser Asn Tyr Thr Lys Ile Arg Asp Gln Ile Arg Lys Lys Tyr Ser Asp
211                      355                      360                      365
214 Trp Asp Ser Phe Ala Leu Pro Leu Gly Arg Ile Ser Glu Tyr Ser Ala
215      370                      375                      380
218 Leu Arg Lys Leu Met Val Glu Lys Tyr Lys Ile Tyr Glu Ser Ser Phe
219 385                      390                      395                      400
222 Asp Arg Arg Gln Ala Ala Pro Arg Phe Val Ile Lys Pro Gln Ser Ala
223                      405                      410                      415
226 Phe Cys Tyr Glu Gly Gln Ser Val Lys Phe Tyr Cys Arg Val Ile Ala
227                      420                      425                      430
230 Val Ala Gln Pro Thr Leu Ser Trp Phe His Asn Asn Glu Glu Leu Arg
231      435                      440                      445
234 Gln Ser Val Lys Phe Met Lys Arg Tyr Ala Gly Glu Asp Tyr Thr Phe
235      450                      455                      460
238 Ile Ile Asn Arg Ala Lys Leu Asp Asp Arg Gly Glu Tyr Ile Ile Arg
239 465                      470                      475                      480
242 Ala Glu Asn Thr Tyr Gly Tyr Arg Glu Glu Val Val Phe Leu Asn Val
243                      485                      490                      495
246 Gln Pro Leu Pro Lys Ala Ala Pro Val Tyr Arg His Glu Val Gln Gln
247      500                      505                      510
250 Val Arg Arg Arg Glu Pro Leu Ala Asn Thr Tyr Tyr Ile Glu Glu Lys
251      515                      520                      525
254 Glu Ser Ala Pro Asn Phe Thr Phe Leu Leu Arg Pro Arg Val Ile Gln
255      530                      535                      540
258 Ile His Gln Thr Cys Lys Leu Leu Cys Cys Leu Ser Gly Thr Pro Ile
259 545                      550                      555                      560
262 Pro Thr Ile Gln Trp Phe Arg Gly Thr Lys Glu Leu Ser Lys Arg Asp
263                      565                      570                      575
266 Tyr Thr Ile Thr His Thr Asp Gly Val Ile Thr Leu Glu Ile Ile Asp
267      580                      585                      590
270 Cys Lys Pro Glu Asp Ser Gly Lys Tyr Arg Cys Val Ala Thr Asn Val

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271          595          600          605
274 His Gly Thr Asp Glu Thr Ser Cys Val Val Ile Val Glu Gly Thr Glu
275          610          615          620
278 Gln Ser Gln Glu Gln Ala Glu Leu Ser His Asn Leu Leu His Ser Asp
279 625          630          635          640
282 Arg Arg Tyr Thr Asp Gln His His Phe Arg Pro Ala Pro Thr Val Ile
283          645          650          655
286 Thr Lys Arg Thr Ala Ile Thr Ser Asn Val His Gly Ser Ser Ser Val
287          660          665          670
290 Ser Ser Asn Gln Ser Ile Thr Thr Asn Ser Ser Thr Lys Ile Ser Asp
291          675          680          685
294 Thr Thr Val Thr Ser Thr Asp Arg Lys Ser Val Lys Lys Tyr Gly Asn
295          690          695          700
298 Lys Leu Asn Ala Ile Gly Ser Pro Ser Arg Ser Arg Ser Ser Thr Lys
299 705          710          715          720
302 Glu Leu Arg Leu Ser Pro Asp Glu Ala Met Cys Pro Pro Asp Phe Ser
303          725          730          735
306 Thr Arg Leu Val Asp Thr Ser Val Asn Asp Gly Gln Ser Leu Glu Leu
307          740          745          750
310 Val Cys Lys Val Thr Gly Asp Phe Glu Pro Gln Ile Thr Trp Leu Lys
311          755          760          765
314 Asn Gly Lys Ala Ile Ser Ser Ser Asn Val Leu Asp Leu Lys Tyr Lys
315          770          775          780
318 Asn Arg Leu Ala Thr Leu Lys Ile Asn Glu Val Phe Pro Glu Asp Ala
319 785          790          795          800
322 Gly Glu Tyr Ile Cys Lys Ala Thr Asn Ser Leu Gly Met Lys Glu Thr
323          805          810          815
326 Ser Cys Lys Leu Thr Val Lys Ala Val Asp Val Ser Lys Asn Lys Ser
327          820          825          830
330 Arg Asn Asp Leu Pro Pro Val
331          835
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336 <212> TYPE: DNA
337 <213> ORGANISM: Artificial Sequence
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Synthetic Construct
342 <400> SEQUENCE: 3
343 agtggacagc gcaattatca
346 <210> SEQ ID NO: 4
347 <211> LENGTH: 21
348 <212> TYPE: DNA
349 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
352 <223> OTHER INFORMATION: Synthetic Construct
354 <400> SEQUENCE: 4
355 gttaccgtag ccgatgtcag a
358 <210> SEQ ID NO: 5
359 <211> LENGTH: 21

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RAW SEQUENCE LISTING

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Input Set : A:\FMC-ADV-009.ST25.txt

Output Set: N:\CRF4\02162006\J528631.raw

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361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
364 <223> OTHER INFORMATION: Synthetic Construct
366 <400> SEQUENCE: 5
367 gaatttagag tgtacgctga a 21
370 <210> SEQ ID NO: 6
371 <211> LENGTH: 20
372 <212> TYPE: DNA
373 <213> ORGANISM: Artificial Sequence
375 <220> FEATURE:
376 <223> OTHER INFORMATION: Synthetic Construct
378 <400> SEQUENCE: 6
379 tactggaggc aagtcgtttc 20
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,631

DATE: 02/16/2006

TIME: 12:47:57

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